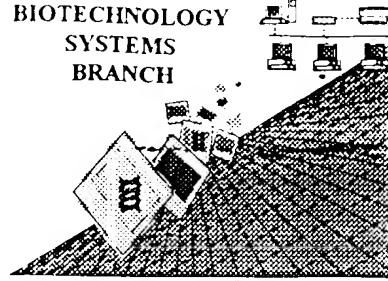




BIOTECHNOLOGY
SYSTEMS
BRANCH



0500

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/670,756

Source: OIPE

Date Processed by STIC: 10/4/2000

COPY

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard SEQ-1.

Checker Version 3.0 replaces the previous DOS-based version of Checker and the UK implement. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/670,756

| ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE | |
|--|---|
| 1 <input type="checkbox"/> Wrapped Nucleics | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". |
| 2 <input type="checkbox"/> Wrapped Aminos | The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping". |
| 3 <input type="checkbox"/> Incorrect Line Length | The rules require that a line not exceed 72 characters in length. This includes spaces. |
| 4 <input type="checkbox"/> Misaligned Amino Acid Numbering | The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers. |
| 5 <input type="checkbox"/> Non-ASCII | This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed. |
| 6 <input type="checkbox"/> Variable Length | Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing. |
| 7 <input type="checkbox"/> PatentIn ver. 2.0 "bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 8 <input type="checkbox"/> Skipped Sequences (OLD RULES) | Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES" response to include the skipped sequence(s). |
| 9 <input type="checkbox"/> Skipped Sequences (NEW RULES) | Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <210> sequence id number <400> sequence id number 000 |
| 10 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 11 <input type="checkbox"/> Use of <213>Organism (NEW RULES) | Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response. The presence of <213> in the sequence listing is mandatory. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown". Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1 823 of new Rules) |
| 13 <input type="checkbox"/> PatentIn ver. 2.0 "bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This function is buggy. Instead, please use "File Manager" or any other means to copy file to floppy disk. |

OIPE

P6
P1

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/670,756

DATE 10/04/2006
TIME 10:17:54

Input Set A:\seqlist.txt
Output Set N:\CRF3\10042000\1670756.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Rhodes, Kenneth
4 Betty, Maria
5 Ling, Huai-Ping
6 An, Wengqian
8 <120> TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
10 <130> FILE REFERENCE: MNI-0'UCP1
12 <140> CURRENT APPLICATION NUMBER: US/09/670,756
13 <141> CURRENT FILING DATE: 2000-09-27
15 <150> PRIOR APPLICATION NUMBER: USSN 60/110,277
16 <151> PRIOR FILING DATE: 1998-11-30
18 <150> PRIOR APPLICATION NUMBER: USSN 60/110,033
19 <151> PRIOR FILING DATE: 1998-11-25
21 <150> PRIOR APPLICATION NUMBER: USSN 60/109,333
22 <151> PRIOR FILING DATE: 1998-11-20
24 <150> PRIOR APPLICATION NUMBER: USSN 69,298,731
25 <151> PRIOR FILING DATE: 1999-04-23
27 <150> PRIOR APPLICATION NUMBER: USSN 69,350,614
28 <151> PRIOR FILING DATE: 1999-07-09
30 <150> PRIOR APPLICATION NUMBER: USSN 69,350,874
31 <151> PRIOR FILING DATE: 1999-07-09
33 <150> PRIOR APPLICATION NUMBER: USSN 69,400,492
34 <151> PRIOR FILING DATE: 1999-09-21
36 <150> PRIOR APPLICATION NUMBER: USSN 69,399,913
37 <151> PRIOR FILING DATE: 1999-09-21
39 <150> PRIOR APPLICATION NUMBER: PCT/US99/27428
40 <151> PRIOR FILING DATE: 1999-11-19
43 <160> NUMBER OF SEQ ID NOS: 73
45 <170> SOFTWARE: PatentIn Ver 2.0
47 <210> SEQ ID NO: 1
48 <211> LENGTH: 1463
49 <212> TYPE: DNA
50 <213> ORGANISM: Homo sapiens
52 <220> FEATURE:
53 <221> NAME/KEY: CDS
54 <222> LOCATION: (225) ..(872)
56 <400> SEQUENCE: 1
58 gaatagcccc ctttcaactt ttagtccttgc catgtgcgggg gctgaagaag gaagccagaa 60
60 gctcttcgtt ctcgccttca cgttttgatua ataccaaaatc gcaagggcgcgc tgcggggcgc 120
62 tttttcttcc tccaaatccatc agtagaaaaa ccacggggat ttctttccat ggttaggggag 180
64 gggccggggcc cggggtrccca actcgccttc aatgttttgc tggc atq ggg gcc atc 236
65 Met Gly Ala Val
66 1
68 atg ggc acc ttc tca tct ctc taa acc aat cttt gaa ccc tcc aaa 284
69 Met Gly Thr Phe Ser Ser Leu Glu Thr Lys Glu Arg Arg Pro Ser Lys
70 5 10 15 20
72 gat aag att gaa gat gaa cttt gaa atq acc atq gtt tgc cat cgg ccc 332
73 Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val Cys His Arg Pro

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/670,756

DATE: 10/04/2000
TIME: 22:17:54

Input Set A:\seqlist.txt
Output Set: N:\CRF3\10042000\I670756.raw

| | | | | |
|-----|---|-----|-----|------|
| 74 | 25 | 30 | 35 | |
| 76 | gaa gta ctg gaa caa ctc gag gac cag acc aac ttc acc aag aag gag | | | 380 |
| 77 | Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg Glu | | | |
| 78 | 40 | 45 | 50 | |
| 80 | ctg caa gtc ctt tat cta ggc ttc aaa aat gag ttc ccc aat ggt gtt | | | 428 |
| 81 | Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly Val | | | |
| 82 | 55 | 60 | 65 | |
| 84 | gtc aac gaa gac aca ttc aag caa atc tat gtc caa ttt ttc ctc cat | | | 476 |
| 85 | Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro His | | | |
| 86 | 70 | 75 | 80 | |
| 88 | gaa gat gcc aca tcc tat gcc cat tac ctc ttc aat gcc ttc gac acc | | | 524 |
| 89 | Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp Thr | | | |
| 90 | 85 | 90 | 95 | 100 |
| 92 | act caa gca ggc tcc ggg aag ttc gag gac ttt gta aat gtc atg tcc | | | 572 |
| 93 | Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu Ser | | | |
| 94 | 105 | 110 | 115 | |
| 96 | att tta ttg aca gga act gtc cac gag aaa cta aat tgg aca ttt aat | | | 620 |
| 97 | Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe Asn | | | |
| 98 | 100 | 105 | 110 | 115 |
| 100 | tgg taa gac att aat aat gaa tac aat aat aat gat gaa atg atg | | | 668 |
| 101 | Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met Met | | | |
| 102 | 105 | 110 | 115 | |
| 104 | gac att gtc aca gca ate tat gac atg atg ggg aaa tat aca tat cct | | | 715 |
| 105 | Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr Pro | | | |
| 106 | 150 | 155 | 160 | |
| 108 | gtg ctc aaa gag gac act cca agg cag cat gtg gac gtc ttc ttc cag | | | 764 |
| 109 | Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe Gln | | | |
| 110 | 165 | 170 | 175 | 180 |
| 112 | aaa atg gac aaa aat aaa gat ggc atc gta act tta gat gaa ttt ctt | | | 812 |
| 113 | Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe Leu | | | |
| 114 | 185 | 190 | 195 | |
| 116 | gaa tca tgg cag gag gac aac atc atg agg tct ctc cag ctg ttt | | | 860 |
| 117 | Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu Phe | | | |
| 118 | 200 | 205 | 210 | |
| 120 | caa aat gtc atg taactggta cactcagccca ttcagcttc agagacattg | | | 912 |
| 121 | Gln Asn Val Met | | | |
| 122 | 215 | | | |
| 124 | tactaaacaa ccacctaacc accctgatct gcccgggttc tgatttaca caccacactct | | | 972 |
| 126 | tggacacaa acacccatcta cacttggaa gaattctctgt ctgaagactt tctttatggaa | | | 1032 |
| 128 | cccaagcatca tgggtgttc tctctgttgc ccaactcttc ctcttttttc ttcttgagaa | | | 1092 |
| 130 | aaatggatg aaatggatg ttgttttggaa agcatgtca ttccttcaca ctgtgtccct | | | 1152 |
| 132 | atggaaaggcc tctctgttca agcttaaca gtatgtcaca aaatatgtctt cttacgtgc | | | 1212 |
| 134 | cccaagccac tgcctccaag tcaggcagac ctgggtgaat ctggaaagaa gaggacccgt | | | 1272 |
| 136 | cccaagatgca caccatctt gatgtcttcc caaaaccaatg tgcctgttcc ttttttttgc | | | 1332 |
| 138 | ttggaaatggatg ttggatgttcc caaaaccaatg tgcctgttcc ttttttttgc | | | 1392 |
| 140 | cacccatcaa cttatgtggg ataggactgtt atttttttttgc atggatgttcc ttttttttgc | | | 1452 |
| 142 | aaactgcacc g | | | 1465 |
| 145 | <210> SEQ ID NO: 2 | | | |
| 146 | <211> LENGTH: 216 | | | |

RAW SEQUENCE LISTING DATE: 10/04/2000
 PATENT APPLICATION US/09/670,756 TIME: 22 17 54

Input Set: A:\seqlist.txt
 Output Set: N:\CRF3\10042000\I670756.raw

147 <212> TYPE: PRT
 148 <213> ORGANISM: Homo sapiens
 150 <406> SEQUENCE 2
 151 Met Gly Ala Val Met Gly Thr Phe Ser Ser Leu Gin Thr Lys Gln Arg
 152 1 5 10 15
 153 5 10 15
 154 Arg Pro Ser Lys Asp Lys Ile Glu Asp Glu Leu Glu Met Thr Met Val
 155 20 25 30
 156 Cys His Arg Pro Glu Gly Leu Glu Leu Glu Ala Gln Thr Asn Phe
 157 35 40 45
 158 40 45
 159 Thr Lys Arg Glu Ile Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
 160 50 55 60
 161 55 60
 162 Pro Ser Gly Val Val Asn Glu Asp Thr Phe Lys Gln Ile Tyr Ala Gln
 163 65 70 75 80
 164 70 75 80
 165 Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
 166 85 90 95
 167 85 90 95
 168 Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
 169 100 105 110
 170 105 110
 171 Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg
 172 115 120 125
 173 115 120 125
 174 Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
 175 130 135 140
 176 135 140
 177 130 135 140
 178 Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
 179 145 150 155 160
 180 145 150 155 160
 181 Tyr Thr Tyr Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp
 182 165 170 175
 183 165 170 175
 184 Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu
 185 180 185 190
 186 180 185 190
 187 Asp Glu Phe Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser
 188 195 200 205
 189 195 200 205
 190 Leu Gln Leu Phe Gln Asn Val Met
 191 210 215
 192 210 215
 193 <210> SEQ ID NO: 3
 194 <211> LENGTH: 1856
 195 <212> TYPE: DNA
 196 <213> ORGANISM: Rattus sp.
 200 <220> FEATURE:
 201 <221> NAME/KEY: CDS
 202 <222> LOCATION: (300)..(1034)
 204 <400> SEQUENCE: 3
 205 ggcacacaaac ccctggattc ttccggagaat atgcgtggat gtgttgccaa ttattttttc 60
 206 tcttggctag cagatgttta gggactgggtt aagcctttgg agaaatttacc ttagaaaaac 120
 207 gggaaataaa aagcaaaagat taccatqaat tgcaagatata cctagcaatt gcaaggtagq 180
 208 aggagagagg tggaggggcg 240
 209 tggggaaat aaccctgcac ttggaaacagc ggcggaaagaaq cgcgattttc cagctttaa 299
 210 atg cct gcc qtc gtt ctg ctt gcc tac ccc gca acq gag atq ttg acc 347
 211 Met Pro Ala Arg Val Leu Ala Tyr Phe Gly Thr Glu Met Leu Thr
 212 1 5 10 15
 213 5 10 15
 214 cag ggc gag tct gaa ggg ctc cag acc ttg ggg ata gta utr qtc ct 395
 215 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/670,756 DATE: 10/01/2000
TIME 22 17:54

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\10042000\I670756.raw

| | | | | |
|-----|---|----|----|------|
| 221 | 20 | 25 | 30 | |
| 222 | tgt tcc tct ctg aaa cta ctg cac tac ctc ggg ctg att gag ttg tcc | | | 145 |
| 223 | Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser | | | |
| 224 | 35 40 45 | | | |
| 225 | gat gac aag atc gag gat gat ctg gaa atg acc atg gtt tgc cat cgg | | | 491 |
| 226 | Asp Asp Lys Ile Glu Asp Asp Asp Leu Glu Met Thr Met Val Cys His Arg | | | |
| 227 | 50 55 60 | | | |
| 228 | cct gaa gga ctg gag cag ctt gag gca cau acq aac ttc acc aag aga | | | 539 |
| 229 | Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg | | | |
| 230 | 65 70 75 80 | | | |
| 231 | gaa ctg caa gtc ctt tac cgg gga ttc aaa aac gag tgc ccc agt ggt | | | 587 |
| 232 | Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly | | | |
| 233 | 85 90 95 | | | |
| 234 | gtg gtt aac gaa gag aca ttc aag cag atc tac tac gct cag ttt ttc ctt | | | 639 |
| 235 | Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro | | | |
| 236 | 100 105 110 | | | |
| 237 | cat gga gat gcc agc aca tac gca cat tac ctc ttc aat gcc ttc gac | | | 683 |
| 238 | His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp | | | |
| 239 | 115 120 125 | | | |
| 240 | acc acc caa aca ggc tct gta aag ttc gag gac ttt gtg act gct ctt | | | 731 |
| 241 | Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu | | | |
| 242 | 130 135 140 | | | |
| 243 | tcg att tta ctg aqa gga aog gtc cat gaa aaa ctg agg tgg acq ttt | | | 779 |
| 244 | Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe | | | |
| 245 | 145 150 155 160 | | | |
| 246 | aat ttg tac gac atc aat aaa gac ggc tac ata aac aaa gag gag atg | | | 827 |
| 247 | Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met | | | |
| 248 | 165 170 175 | | | |
| 249 | atg gac ata gtg aaa gcc atc tat gac atg atg ggg aaa tac acc tat | | | 875 |
| 250 | Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr | | | |
| 251 | 180 185 190 | | | |
| 252 | cct gtg ctc aaa gag gac act ccc agg cag cac gtg gac gtc ttc ttc | | | 923 |
| 253 | Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe | | | |
| 254 | 195 200 205 | | | |
| 255 | cag aaa atg gat aaa aat aaa gat ggc att gta acg tta gac gaa ttt | | | 971 |
| 256 | Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe | | | |
| 257 | 210 215 220 | | | |
| 258 | ctc gag tcc tgt cag gag gat gac aac atc atg agg tct cta cag ctg | | | 1019 |
| 259 | Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu | | | |
| 260 | 225 230 235 240 | | | |
| 261 | tcc caa aat gtc atg taactgagga cactggccat cctgctctca gagacactga | | | 1074 |
| 262 | Phe Gln Asn Val Met | | | |
| 263 | 245 | | | |
| 264 | caaacacctc aatgcctga tctgccttg tttcagttt acacatcaac tctggggaca | | | 1134 |
| 265 | gaaataacctt ttacactttt gaaagatttc ctgtgtttttt aacctggcac 1194 | | | |
| 266 | cgatggctc aqtcctgtat tgcctacttc tcttccttcc tcccttttgg aaaaaacgaaac 1254 | | | |
| 267 | tggaaatccgaa agttttttt gaaagcatgc ccaatcttcc atatgtgttc tgcctgtgg 1314 | | | |
| 268 | aaggccccc tgcgttggatctaaacaaatggatggacatgtttt tcttgtata cagatcccc 1374 | | | |
| 269 | actcaatgtcc tctaaatgtca gcaatcccttca accaaatgtt caccatcc 1434 | | | |

RAW SEQUENCE LISTING
 PATENT APPLICATION US/09/670,756 DATE: 10/04/2000
 FILED: 09/09/2000 TIME: 22:17:54

Input Set: A:\seqlist.txt
 Output Set: N:\CRF3\10042000\I670756.raw

293 ccatggcctc ccaagccaat gtgcctgttt ctcttcctct cgtggaaaga aagaacgc 1494
 294 tacagagcac tttagactta ccatqaadat acgtggaaagc gcagcaccta acacatgtag 1551
 295 autaggactg aatttataag cttgggtgtt tcagatgtg cttttttttttt atgtcatttt 1611
 299 tttttccaga ggttaggact aataatttc cccactatgc acctacatgc atagaacaaq 1674
 301 tctttttaaca catccaggag ggaacccgtt gcccactgtgt ctatcccttc tctccatccc 1731
 303 ctgtcaagc ccacgactgc atgtctcttc cggaaaggcc agaatgcctg tggaaatgtg 1794
 305 taacttttat accctgttat aatcaataaa cagaactatt tcgtacaaaa aaaaaaaaaa 1854
 307 aa 1856
 310 <210> SEQ ID NO: 4
 311 <211> LENGTH: 245
 312 <212> TYPE: PRT
 313 <213> ORGANISM: *Rattus* sp.
 315 100 SEQUENCE: 4
 316 Met Pro Ala Arg Val Leu Ala Tyr Pro Gly Thr Glu Met Leu Thr
 317 1 5 10 15
 318 Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val Val Val Leu
 319 20 25 30
 320 22 Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile Asp Leu Ser
 321 35 40 45
 322 Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val Cys His Arg
 323 50 55 60
 324 Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe Thr Lys Arg
 325 65 70 75 80
 326 Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys Pro Ser Gly
 327 85 90 95
 328 Val Val Asn Glu Glu Thr Phe Lys Gln Ile Tyr Ala Gln Phe Phe Pro
 329 100 105 110
 330 His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn Ala Phe Asp
 331 115 120 125
 332 340 Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val Thr Ala Leu
 333 130 135 140
 334 Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Arg Trp Thr Phe
 335 145 150 155 160
 336 Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys Glu Glu Met
 337 165 170 175
 338 Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys Tyr Thr Tyr
 339 180 185 190
 340 Pro Val Leu Lys Glu Asp Thr Pro Arg Gln His Val Asp Val Phe Phe
 341 195 200 205
 342 Gln Lys Met Asp Lys Asn Lys Asp Gly Ile Val Thr Leu Asp Glu Phe
 343 210 215 220
 344 Leu Glu Ser Cys Gln Glu Asp Asp Asn Ile Met Arg Ser Leu Gln Leu
 345 225 230 235 240
 346 Phe Gln Asn Val Met
 347 245
 348 <210> SEQ ID NO: 5
 349 <211> LENGTH: 1907
 350 <212> TYPE: DNA
 351 <213> ORGANISM: *Mus musculus*

09/06/70, 756

6

<210> 12
<211> 203
<212> PRT
<213> Rattus sp.

<400> 12
Met Leu Thr Gln Gly Glu Ser Glu Gly Leu Gln Thr Leu Gly Ile Val
1 5 10 15
Val Val Leu Cys Ser Ser Leu Lys Leu Leu His Tyr Leu Gly Leu Ile
20 25 30
Asp Leu Ser Asp Asp Lys Ile Glu Asp Asp Leu Glu Met Thr Met Val
35 40 45
Cys His Arg Pro Glu Gly Leu Glu Gln Leu Glu Ala Gln Thr Asn Phe
50 55 60
Thr Lys Arg Glu Leu Gln Val Leu Tyr Arg Gly Phe Lys Asn Glu Cys
65 70 75 80
Pro Ser Gly Val Val Asn Glu Glu Thr Phe Lys (Xaa) Ile Tyr Ala Gln
85 90 95
Phe Phe Pro His Gly Asp Ala Ser Thr Tyr Ala His Tyr Leu Phe Asn
100 105 110
Ala Phe Asp Thr Thr Gln Thr Gly Ser Val Lys Phe Glu Asp Phe Val
115 120 125
Thr Ala Leu Ser Ile Leu Leu Arg Gly Thr Val His Glu Lys Leu Lys
130 135 140
Trp Thr Phe Asn Leu Tyr Asp Ile Asn Lys Asp Gly Tyr Ile Asn Lys
145 150 155 160
Glu Glu Met Met Asp Ile Val Lys Ala Ile Tyr Asp Met Met Gly Lys
165 170 175
Tyr Thr Tyr Leu Val Leu Lys Glu Asp Thr Ser Arg Gln His Val Asp
180 185 190
Val Phe Phe Gln Lys Met Asp Lys Asn Lys Asp
195 200

All item 10
or Error
Summary
Sheet

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION US/09/670,756

DATE: 10/04/2000
TIME: 22:17:55

Input Set : A:\seqlist.txt
Output Set: N:\CRF3\10042000\I670756.raw

L:12 M:270 C: Current Application Number differs. Replaced Application Number
L:13 M:271 C: Current Filing Date differs. Replaced Current Filing Date
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 11
L:883 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 11
L:936 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 12
L:936 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 12
L:936 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 12
L:936 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 12
L:936 M:310 W: (46) "n" or "Xaa" used, Feature required, for SEQ ID# 12
I:3028 M:311 W: (46) "n" or "Xaa" used, for SEQ ID# 37
L:3362 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 43
L:3362 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 43
L:3362 M:340 W: (46) "n" or "Xaa" used, Feature required, for SEQ ID# 43
L:3365 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 43
L:3365 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 43
M:340 Repeated in SeqNo=43